

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 12, 2004, 15:54:54 ; Search time 41 Seconds  
(without alignments)  
1869.308 Million cell updates/sec

Title: US-09-809-827-31  
Perfect score: 297  
Sequence: 1 MGDHWSFLKDFLAGAVAAA.....LRMGAGFVLVLYDEIKKYV 297

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 30

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	81	27.3	298	6	O46373 oryctolagus
2	80	26.9	298	11	Q8BV19 mus musculus
3	48	16.2	170	6	Q9X569 sus scrofa
4	48	16.2	254	11	Q8BKQ5 mus musculus
5	41	13.8	298	13	Q8JH10 brachydanio
6	39	13.1	298	6	Q8SDH5 bos taurus
7	39	13.1	298	13	Q9YIC4 rana rugosa
8	39	13.1	298	13	Q9PRH2 rana rugosa
9	39	13.1	298	13	Q919M9 xenopus lae
10	39	13.1	298	13	Q9PRH1 rana rugosa
11	39	13.1	298	13	Q8AYM3 gallus gall
12	39	13.1	317	13	Q91336 rana sylvat
13	37	12.5	312	5	Q81RA0 drosophila
14	34	11.4	307	5	O62526 drosophila
15	34	11.4	313	5	Q21103 caenorhabdi
16	34	11.4	313	5	P91410 caenorhabdi

17	32	10.8	300	5	O45865	caenorhabdi
18	32	10.8	300	5	Q17407	caenorhabdi
19	31	10.4	315	4	Q9H0C2	homo sapien
20	30	10.1	288	5	O44094	drosophila
21	30	10.1	288	5	O44093	drosophila
22	30	10.1	300	5	Q9NHWS	lucilia cup

ALIGNMENTS

RESULT 1

O46373 ID O46373 PRELIMINARY; PRT; 298 AA.  
AC O46373;  
DT 01-JUN-1998 (Tremblrel. 06, Created)  
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE ADP/ATP translocase.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Skeletal muscle;  
RA Yamaguchi N., Kasai M.;  
RT "Identification of a 30kDa calsequestrin-binding protein, which  
regulates calcium release from sarcoplasmic reticulum of rabbit  
skeletal muscle.";  
RL J. Biochem. 335:541-547(1998).  
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
DR EMBL; AB009386; BAA23777.1; -.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR InterPro; IPR002067; Mit\_carrier.  
DR InterPro; IPR002030; Mit\_uncoupling.  
DR Pfam; PF00153; mito\_carr; 3.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PRINTS; PR00784; MTUNCOUPLING.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
KW Membrane; Transmembrane; Transport.  
SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 27.3%; Score 81; DB 6; Length 298;  
Best Local Similarity 100.0%; Pred. No. 6.3e-74;  
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	17	VAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLA	76
DB	17	VAAAVSKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLA	76
QY	77	NVIRYFPTQALNFAFKDKYKQ	97
DB	77	NVIRYFPTQALNFAFKDKYKQ	97

RESULT 2

O8BV19 ID Q8BV19 PRELIMINARY; PRT; 298 AA.  
AC Q8BV19;  
DT 01-MAR-2003 (Tremblrel. 23, Created)  
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)  
DE Solute carrier family 25.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Medulla oblongata;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium;

RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573(2002).";  
DR EMBL; AK078077; BAC37117.1; -. F94C89009836710B CRC64;  
SQ SEQUENCE 298 AA; 32904 MW; 794C89009836710B CRC64;  
Query Match 26.9%; Score 80; DB 11; Length 298;  
Best Local Similarity 100.0%; Pred. No. 6.7e-73; Indels 0; Gaps 0;  
Matches 80; Conservative 0; Mismatches 0;  
QY 18 AAASKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77  
DB 18 AAASKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77  
QY 78 VIRYPTQALNFAFKDKYKQ 97  
DB 78 VIRYPTQALNFAFKDKYKQ 97  
RESULT 3  
Q9XS69 PRELIMINARY; PRT; 170 AA.  
AC Q9XS69  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Adenine nucleotide translocator 1 (Fragment).  
GN ANTL.  
OS Sus scrofa domestica (domestic pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9825;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99269917; PubMed=10337623;  
RA Larsen N.J., Marklund S., Kelly K.A., Malek M., Tuggle C.K., Yerle M.,  
RA Rothschild M.F.;  
RT "New insights into porcine-human syntenic conservation.";  
RL Mamm. Genome 10:488-491(1999).  
DR EMBL; AF05633; AAD20940.1; -.  
DR InterPro; IPR001993; Mitoch. carrier.  
DR InterPro; IPR002067; Mit. carrier.  
DR Pfam; PF00153; mito carr. 2.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 1.  
FT NON TER 1  
FT NON TER 170  
SQ SEQUENCE 170 AA; 18769 MW; C389C14D3C464CB9 CRC64;  
Query Match 16.2%; Score 48; DB 6; Length 170;  
Best Local Similarity 100.0%; Pred. No. 1.9e-40;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 99 FLGGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146  
DB 38 FLGGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 85  
RESULT 4  
Q8BKQ5 PRELIMINARY; PRT; 254 AA.  
AC Q8BKQ5  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Solute carrier family 25.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573(2002).";  
DR EMBL; AK051172; BAC34543.1; -. D85A79F58F2E3B96 CRC64;  
SQ SEQUENCE 254 AA; 27931 MW; D85A79F58F2E3B96 CRC64;  
Query Match 16.2%; Score 48; DB 11; Length 254;  
Best Local Similarity 100.0%; Pred. No. 2.7e-40;  
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 99 FLGGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146  
DB 99 FLGGVDRHKQFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146  
RESULT 5  
Q8JH10 PRELIMINARY; PRT; 298 AA.  
AC Q8JH10  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Solute carrier family 25 member 5 protein.  
GN SLC35A5.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22035902; PubMed=12006978;  
RA Golling G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,  
RA Burgess S., Haldi M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,  
RA Hopkins N.;  
RT "Insertional mutagenesis in zebrafish rapidly identifies genes  
RT essential for early vertebrate development.";  
RL Nat. Genet. 31:135-140(2002).  
DR EMBL; AF506216; AAM34660.1; -.  
DR InterPro; IPR001993; Mitoch. carrier.  
DR InterPro; IPR002067; Mit. carrier.  
DR InterPro; IPR002030; Mit. uncoupling.  
DR Pfam; PF00153; mito carr. 3.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PRINTS; PR00784; MTUNCOUPLING.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
SQ SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;  
Query Match 13.8%; Score 41; DB 13; Length 298;  
Best Local Similarity 100.0%; Pred. No. 4.3e-33;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 56 DCVVRIPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYK 96  
DB 56 DCVVRIPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYK 96  
RESULT 6  
Q8SQH5 PRELIMINARY; PRT; 298 AA.  
AC Q8SQH5  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Adenine nucleotide translocator 2.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.

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OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
RT identification of possible amino acids that determine functional
RL Mitochondrion 1:371-379(2002).
DR EMBL; AB065433; BAB84673.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;

Query Match 13.1%; Score 39; DB 6; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 7
Q9YIC4 PRELIMINARY; PRT; 298 AA.
AC Q9YIC4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes of
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008457; BAA36507.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 8
Q9PRH2 PRELIMINARY; PRT; 298 AA.
AC Q9PRH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes of
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008460; BAA36510.1; -.
DR EMBL; AB008458; BAA36508.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 9
Q9I9M9 PRELIMINARY; PRT; 298 AA.
AC Q9I9M9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocase.
GN ANTI.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT Dynamic Patterns of Expression During Development."
RL Submitted (FEB-2000) to the EMBL/Genbank/DBS databases.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF231347; AAF63471.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
Db 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADV 146
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RESULT 10
Q9PRH1 PRELIMINARY; PRT; 298 AA.
AC Q9PRH1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorph sex chromosomes
RT Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -.
DR EMBL; AB008456; BAA36506.1; -.
DR EMBL; AB008461; BAA36511.1; -.
DR EMBL; AB008462; BAA36512.1; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR Membrane; Transmembrane; Transport.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; 50E23AD56F48D36 CRC64;

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146
Db |||||
108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 11
Q8AYM3 PRELIMINARY; PRT; 298 AA.
AC Q8AYM3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP antiporter.
GN AVANT.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazew R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,

Query Match 13.1%; Score 39; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.8e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146
Db |||||
108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 12
Q91336 PRELIMINARY; PRT; 317 AA.
ID Q91336
AC Q91336
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana sylvatica (Wood frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=45438;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97398141; PubMed=9256066;
RA Cai Q., Greenway S.C., Storey K.B.;
RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
RT in wood frogs under freezing stress."
RL Biochim. Biophys. Acta 1353:69-78(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cai Q., Storey K.B.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; U44832; AAA97882.2; -.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR Membrane; Transmembrane; Transport.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

Query Match 13.1%; Score 39; DB 13; Length 317;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146
Db |||||
108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 13
Q8IRA0 PRELIMINARY; PRT; 312 AA.
ID Q8IRA0
AC Q8IRA0
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG16944-PC.
GN SESB.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazew R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasner K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Klamm P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RA "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,  
RA Banon J., An H., Baldwin D., Bonzon J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirekas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RT "Sequencing of Drosophila melanogaster genome."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RN SEQUENCE FROM N.A.  
RP Miera S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RT "Annotation of Drosophila melanogaster genome."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RN SEQUENCE FROM N.A.  
RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RN SEQUENCE FROM N.A.  
RP FlyBase;  
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003484; AAN09267.1; -;  
SQ SEQUENCE 312 AA; 34214 MW; 76D5834E74E168DF CRC64;

Query Match 12.5%; Score 37; DB 5; Length 312;  
Best Local Similarity 100.0%; Pred. No. 5.5e-29;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGSGAAGATSLCFVYPLDFARTRLAAD 144  
DB 123 QFWRYFAGNLAGSGAAGATSLCFVYPLDFARTRLAAD 159  
RESULT 14  
O62526 PRELIMINARY; PRT; 307 AA.  
ID O62526;  
AC O62526;  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE ANT2 protein.  
GN ANT2 OR CGI683.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Allwell J.F., Agbayani A., An H.-J., Andrews-Efannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasner K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merklov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=OREGON-R;  
RC Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003484; AAF47956.1; -;  
DR EMBL; Y10618; CAA71629.1; -;  
DR FlyBase; Fgn002511; Ant2.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR InterPro; IPR002067; Mit\_carrier.  
DR Pfam; PF00153; mito\_carr; 3.

DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH CARRIER; 2.  
SQ SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061C0C CRC64;

Query Match 11.4%; Score 34; DB 5; Length 307;  
Best Local Similarity 100.0%; Pred.No. 6.4e-26;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146  
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Db 123 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 156

## RESULT 15

Q211103  
ID Q21103 PRELIMINARY; PRT; 313 AA.  
AC Q21103,  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
DE K01H12.2 protein.  
GN K01H12.2  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA McMurray A.A.;  
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
investigating biology.";  
RL Science 282:2012-2018(1998).  
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.  
DR EMBL; Z68218; CAA92472.1; -.  
DR WormPep; K01H12.2; CE03454.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mito\_carr; 3.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH CARRIER; 3.  
KW Membrane; Transmembrane; Transport.  
SQ SEQUENCE 313 AA; 34384 MW; D1E455DDB463C984 CRC64;

Query Match 11.4%; Score 34; DB 5; Length 313;  
Best Local Similarity 100.0%; Pred.No. 6.4e-26;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146  
|||  
Db 130 FAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 163

Search completed: February 12, 2004, 15:57:13  
Job time : 42 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 12, 2004, 15:54:54 ; Search time 17 Seconds  
(without alignments)  
821.584 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 297  
Sequence: 1 MGDHAWFLKDFLAGAVAA.....LRGMGAFVLVLYDEIKKVV 297

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 30

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	130	43.8	298	1 ADT1_HUMAN	P12235 homo sapien
2	80	26.9	298	1 ADT1_MOUSE	P48962 mus musculus
3	80	26.9	298	1 ADT1_RAT	Q05962 rattus norv
4	76	25.6	297	1 ADT1_BOVIN	P02722 bos taurus
5	39	13.1	298	1 ADT2_HUMAN	P05141 homo sapien
6	39	13.1	298	1 ADT2_MOUSE	P51881 mus musculus
7	39	13.1	298	1 ADT2_RAT	Q09073 rattus norv
8	39	13.1	298	1 ADT3_BOVIN	P32007 bos taurus
9	39	13.1	298	1 ADT3_HUMAN	P12236 homo sapien
10	37	12.5	299	1 ADT_DROME	Q26365 drosophila

#### ALIGNMENTS

RESULT 1  
ID ADT1\_HUMAN STANDARD; PRT; 298 AA.  
AC P12235;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).  
DE SLC25A4 OR ANT1.  
GN Homo sapiens (Human).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89236396; PubMed=2541251;  
RA Cozens A.L., Runswick M.J., Walker J.E.;

RT "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";  
RL J. Mol. Biol. 206:261-280(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89340499; PubMed=2547778;  
RA Li K., Warner C.K., Hodges J.A., Minoshima S., Kudoh J., Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;  
RA "A human muscle adenine nucleotide translocator gene has four exons, RT is located on chromosome 4, and is differentially expressed.";  
RL J. Biol. Chem. 264:13998-14004(1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88041149; PubMed=2823286;  
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;  
RA "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader peptide, divergence from a fibroblast translocator cDNA, RT and coevolution with mitochondrial DNA genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Eye;  
MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 1-37 FROM N.A.  
RX TISSUE=Liver;  
MEDLINE=88124845; PubMed=2829183;  
RA Houldsworth J., Attardi G.;  
RA "Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";  
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).  
RN [6]  
RP VARIANTS PRO PRO-114 AND MET-289.  
RX MEDLINE=20385067; PubMed=10926341;  
RA Kaukonen J., Juselius J.K., Tiranti V., Kyttala A., Zeviani M., Comi G.P., Keranen J., Peltonen L., Suomalainen A.;  
RA "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";  
RL Science 289:782-785(2000).  
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.  
CC -1- SUBUNIT: Homodimer.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.  
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.  
CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant progressive external ophthalmoplegia with various mitochondrial DNA deletions (PEO). Patients with PEO have mitochondrial myopathy, progressive external ophthalmoplegia, and other abnormalities associated with multiple different deletions of mitochondrial DNA.  
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.  
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02966; AAA61223.1; -
DR EMBL; J03593; AAA36751.1; -
DR EMBL; J04982; AAA51736.1; -
DR EMBL; BC008664; AAH08664.1; -
DR PIR; A44778; A44778.
DR Genew; HGNC:10990; SLC25A4.
DR MIM; 103220; -
DR MIM; 157640; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005739; C:mitochondrion; TAS.
DR GO; GO:0015207; F:adenine transporter activity; TAS.
DR GO; GO:0006091; P:energy pathways; TAS.
DR GO; GO:0000002; P:mitochondrial genome maintenance; TAS.
DR GO; GO:0006832; P:small molecule transport; TAS.
DR InterPro; IPR02067; Mit_carrier.
DR InterPro; IPR02030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Disease mutation.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT VARIANT 114 114 A -> P (IN PRO).
FT VARIANT 289 289 /FTID=VAR_012111.
FT VARIANT 16 16 /FTID=VAR_012112.
FT CONFLICT 147 149 G -> A (IN REF. 3).
FT CONFLICT 227 227 KGA -> RR (IN REF. 3).
FT CONFLICT 227 227 V -> L (IN REF. 3).
SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAC4E7CFEB CRC64;

Query Match 43.8%; Score 130; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.1e-121;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 VAAVSTAVPIERVKLLIQVHASKQISAQKYGKIIDCVVRIPEQGFSLFWGNLA 76
Db 17 VAAVSTAVPIERVKLLIQVHASKQISAQKYGKIIDCVVRIPEQGFSLFWGNLA 76
QY 77 NVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASGGAAGATSLCFVYPLDF 136
Db 77 NVIRYPTQALNFAFKDKYKQLFLGGVDRHKQFWRYPAGNLASGGAAGATSLCFVYPLDF 136
QY 137 ARTLEAADVG 146
Db 137 ARTLEAADVG 146

RESULT 2
ADTI MOUSE
ID ADTI1 MOUSE STANDARD; PRT; 298 AA.
AC P48962; Q62164;
DT 01-FEB-1996 (Rel. 33, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP

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DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (mANCI).
GN SLC25A4 OR ANT1 OR ANCI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs.";
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Muscle;
RA Laplace C., Costet P.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U27315; AAC52837.1; -
DR EMBL; X74510; CAA52616.1; -
DR EMBL; AF240002; AAF64470.1; -
DR EMBL; BC003791; AAH03791.1; -
DR EMBL; BC026925; AAH26925.1; -
DR PIR; S37210; S37210.
DR MGI; MGI:1353495; Slc25a4.
DR InterPro; IPR002067; Mit_carrier.

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DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARPLING.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 136 136 F -> L (IN REF. 1).
SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match 26.9%; Score 80; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.3e-72;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AAASVTAVAPIERVKLLQVHASKQISAERKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77
DB 18 AAASVTAVAPIERVKLLQVHASKQISAERKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77

QY 78 VIRYPTQALNFAFKDKYKQ 97
DB 78 VIRYPTQALNFAFKDKYKQ 97

RESULT 3
ADT1_RAT
ID ADT1_RAT STANDARD; PRT; 298 AA.
AC Q05962;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochem. Biophys. Acta 1152:192-196 (1993).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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DR EMBL; X61667; CAA43842.1; -.
DR EMBL; D12770; BAA02237.1; -.
DR PIR; I60173; I60173.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARPLING.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 26.9%; Score 80; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.3e-72;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AAASVTAVAPIERVKLLQVHASKQISAERKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77
DB 18 AAASVTAVAPIERVKLLQVHASKQISAERKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77

QY 78 VIRYPTQALNFAFKDKYKQ 97
DB 78 VIRYPTQALNFAFKDKYKQ 97

RESULT 4
ADT1_BOVIN
ID ADT1_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873 (1989).
RN [2]
SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349 (1982).
RN [3]
SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857 (1986).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

```

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CC CC MITOCHONDRIAL INNER MEMBRANE.
CC CC -I- SUBUNIT: Homodimer.
CC CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC CC inner membrane.
CC CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; M131783; AAA30363.1; -.
CC CC EMBL; M24102; AAA30768.1; -.
CC CC PIR; A43646; XWBO.
CC CC InterPro; IPR002067; Mit_carrier.
CC CC InterPro; IPR002030; Mit_uncoupling.
CC CC InterPro; IPR001993; Mitoch_carrier.
CC CC Pfam; PF00153; mito_carr; 3.
CC CC PRINTS; PR00926; MITOCARRIER.
CC CC PRINTS; PR00784; MTUNCOUPLING.
CC CC PROSITE; PS00215; MITOCH_CARRIER; 3.
CC CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC CC Multigene family; Methylation.
CC CC INIT_MET 0
CC CC MOD_RES 0 1 BLOCKED.
CC CC MOD_RES 51 51 METHYLATION (POTENTIAL).
CC CC TRANSMEM 11 28 1 (POTENTIAL).
CC CC TRANSMEM 72 90 2 (POTENTIAL).
CC CC TRANSMEM 116 133 3 (POTENTIAL).
CC CC TRANSMEM 175 194 4 (POTENTIAL).
CC CC TRANSMEM 213 230 5 (POTENTIAL).
CC CC TRANSMEM 272 290 6 (POTENTIAL).
CC CC REPEAT 1 110 1.
CC CC REPEAT 111 207 2.
CC CC REPEAT 208 297 3.
CC CC SEQUENCE 297 AA; 32836 MW; A582D3C4A40AE948 CRC64;

Query Match 25.6%; Score 76; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 7e-68;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVIRIPKEQGLSFWRGNLANVIRY 81
DB 21 SKTAVAPIERVKLLQVQHASKQISAEKQYKGIIDCVIRIPKEQGLSFWRGNLANVIRY 80
QY 82 FPTQALNFAFKDKYKQ 97
DB 81 FPTQALNFAFKDKYKQ 96

RESULT 5
ADT2 HUMAN
ID ADT2 HUMAN STANDARD; PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
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RT RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RL RL cloning and sequence."
RL J. Biol. Chem. 265:16060-16063 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358 (1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
RA Mazzarella R.A., Schlessinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozersky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381 (1988).
CC CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC CC MITOCHONDRIAL INNER MEMBRANE.
CC CC -I- SUBUNIT: Homodimer.
CC CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC CC inner membrane.
CC CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC CC -I- SIMILARITY: Belongs to the mitochondrial carrier family.
CC CC -----
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CC CC -----
CC CC EMBL; M57424; AAA51737.1; -.
CC CC EMBL; J02683; AAA35579.1; -.
CC CC EMBL; L78810; AAB39266.1; -.
CC CC EMBL; AC004000; AAB96347.1; -.
CC CC EMBL; J03591; AAA36749.1; -.
CC CC PIR; A29132; A29132.
CC CC Genew; HGNC:10991; SLC25A5.
CC CC MIM; 300150; -.
CC CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC CC GO; GO:0015207; F:adenine transporter activity; TAS.
CC CC GO; GO:0006832; P:small molecule transport; TAS.
CC CC InterPro; IPR002067; Mit_carrier.
CC CC InterPro; IPR002030; Mit_uncoupling.
CC CC Pfam; PF00153; mito_carr; 3.
CC CC PRINTS; PR00926; MITOCARRIER.
CC CC PRINTS; PR00784; MTUNCOUPLING.
CC CC PROSITE; PS00215; MITOCH_CARRIER; 3.
CC CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC CC Multigene family.
CC CC TRANSMEM 12 29 1 (POTENTIAL).
CC CC TRANSMEM 73 91 2 (POTENTIAL).
CC CC TRANSMEM 117 134 3 (POTENTIAL).
CC CC TRANSMEM 176 195 4 (POTENTIAL).
CC CC TRANSMEM 214 231 5 (POTENTIAL).
CC CC TRANSMEM 273 291 6 (POTENTIAL).
CC CC REPEAT 1 111 1.
CC CC REPEAT 112 208 2.
CC CC REPEAT 209 298 3.
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FT CONFLICT 6 6 V -> L (IN REF. 2).
FT CONFLICT 66 66 G -> E (IN REF. 2).
FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 13.18; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLSGGAAGATSLCFVYPLDFARTRLAADV 146
DB 108 QFWRYFAGNLSGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 6
ADT2 MOUSE STANDARD; PRT; 298 AA.
AC P51881; Q61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
homologs.";
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Costet P., Laplace C.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [4]
RA Laplace C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20432087; PubMed=10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
translocase 1 and 2 genes.";
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC U27316; AAC52838.1; -
DR EMBL; U10404; AAA19009.1; -
DR EMBL; X70847; CAAS0196.1; -
DR EMBL; AF240003; AAF64471.1; -
DR MGD; MG1:1353496; SLC25A5.
DR InterPro; IPR002067; Mit_carrier.
DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF0153; mito_carr; 3.
DR PRINTS; PR00784; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLSGGAAGATSLCFVYPLDFARTRLAADV 146
DB 108 QFWRYFAGNLSGGAAGATSLCFVYPLDFARTRLAADV 146

RESULT 7
ADT2 RAT STANDARD; PRT; 298 AA.
AC Q09073;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
inner membrane.
CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
SKELETAL MUSCLE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC -----
CC EMBL: D12771; BAA02238.1; -.
CC InterPro; IPR002067; Mit_carrier.
CC InterPro; IPR002030; Mit_uncoupling.
CC InterPro; IPR001993; Mitoch_carrier.
CC Pfam; PF00153; Mitoch_carrier.
CC PRINTS; PR00926; MITOCARRIER.
CC PRINTS; PR00784; MTUNCOUPLING.
CC PROSITE; PS00215; MITOCH_CARRIER; 3.
CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
KW TRANSMEM 12 29 1 (POTENTIAL).
KW TRANSMEM 73 91 2 (POTENTIAL).
KW TRANSMEM 117 134 3 (POTENTIAL).
KW TRANSMEM 176 195 4 (POTENTIAL).
KW TRANSMEM 214 231 5 (POTENTIAL).
KW TRANSMEM 273 291 6 (POTENTIAL).
KW REPEAT 1 111 1.
KW REPEAT 112 208 2.
KW REPEAT 209 298 3.
KW SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146
DB 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 8
ADT3_BOVIN
ID ADT3_BOVIN STANDARD; PRT; 298 AA.
AC P32007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP,ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
DE SLC25A6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
CC -|- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -|- SUBUNIT: Homodimer.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -|- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -|- SIMILARITY: Belongs to the mitochondrial carrier family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24103; AAA30769.1; -.
CC PIR; B43646; B43646.
CC InterPro; IPR002067; Mit_carrier.

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DR InterPro; IPR002030; Mit_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
KW TRANSMEM 12 29 1 (POTENTIAL).
KW TRANSMEM 73 91 2 (POTENTIAL).
KW TRANSMEM 117 134 3 (POTENTIAL).
KW TRANSMEM 176 195 4 (POTENTIAL).
KW TRANSMEM 214 231 5 (POTENTIAL).
KW TRANSMEM 273 291 6 (POTENTIAL).
KW REPEAT 1 111 1.
KW REPEAT 112 208 2.
KW REPEAT 209 298 3.
KW SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 13.1%; Score 39; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 5.1e-31;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146
DB 108 QFWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 9
ADT3_HUMAN
ID ADT3_HUMAN STANDARD; PRT; 298 AA.
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP,ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
DE SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89216396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase.";
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Cervix, Eye, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg K.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of *Drosophila melanogaster*";  
RL Science 287:2185-2195(2000).  
RN [5]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Berkeley; TISSUE=Larva, Ovary, and Pupae;  
RX MEDLINE=22426066; PubMed=12537569;  
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,  
RA George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,  
RA Rubin G.M., Celniker S.E.;  
RT "A *Drosophila* full-length cDNA resource";  
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).  
CC -i- FUNCTION: Catalyzes the exchange of ADP and ATP across the  
CC mitochondrial inner membrane.  
CC -i- SUBUNIT: Homodimer (By similarity).  
CC -i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial  
CC inner membrane (By similarity).  
CC -i- DOMAIN: Composed of three homologous domains.  
CC -i- SIMILARITY: Belongs to the mitochondrial carrier family.  
CC -----  
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CC -----  
DR EMBL; S43651; AAB23114.1; -;  
DR EMBL; S71762; AAB31734.3; -;  
DR EMBL; Y10618; CAA71628.1; -;  
DR EMBL; AE003484; AAF47957.1; -;  
DR EMBL; AY060978; AAL2826.1; -;  
DR EMBL; AY070894; AAL48516.1; -;  
DR FlyBase; FBgn0003360; seqB.  
DR GO; GO:0005743; C-mitochondrial inner membrane; IEP.  
DR GO; GO:0006839; P-mitochondrial transport; IMP.  
DR InterPro; IPR001993; Mitoch\_carrier.  
DR Pfam; PF00153; mito\_carr; 2.  
DR PRINTS; PR00926; MITOCARRIER.  
DR PROSITE; PS00215; MITOCH\_CARRIER; 3.  
KW Mitochondrion; Inner membrane; Repeat: Transmembrane; Transport.  
FT TRANSMEM 14 31 1 (POTENTIAL).  
FT TRANSMEM 75 93 2 (POTENTIAL).  
FT TRANSMEM 119 136 3 (POTENTIAL).  
FT TRANSMEM 177 196 4 (POTENTIAL).  
FT TRANSMEM 215 232 5 (POTENTIAL).  
FT TRANSMEM 274 292 6 (POTENTIAL).  
FT CONFLICT 18 19 GI -> QV (IN REF. 1 AND 2).  
FT CONFLICT 81 81 I -> Y (IN REF. 1).  
FT CONFLICT 201 201 MISSING (IN REF. 1 AND 2).  
FT CONFLICT 267 267 G -> A (IN REF. 2).  
FT CONFLICT 268 269 TG -> P (IN REF. 1 AND 2).  
FT CONFLICT 270 270 A -> S (IN REF. 1).  
FT CONFLICT 270 270 A -> C (IN REF. 2).  
SQ SEQUENCE 299 AA; 32909 MW; D51F3E2A70BD59E8 CRC64;  
  
Query Match 12.5%; Score 37; DB 1; Length 299;  
Best Local Similarity 100.0%; Pred. No. 5e-29;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAD 144  
DB 110 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAD 146

Search completed: February 12, 2004, 15:56:19  
Job time : 17 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 12, 2004, 15:55:55 ; Search time 20 Seconds  
(without alignments)  
1428.105 Million cell updates/sec

Title: US-09-809-827-31  
Perfect score: 297  
Sequence: 1 MGDHAWFLKDFLAGAVAAA.....LRGMGAFVLVLYDEIKKYV 297

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 30

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR 76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	130	43.8	298	1	A44778	ADP,ATP carrier pr
2	80	26.9	298	2	S37210	ADP,ATP carrier pr
3	80	26.9	298	2	I60173	adenine nucleotide
4	76	25.6	298	1	XWBO	ADP,ATP carrier pr
5	39	13.1	298	1	A29132	ADP,ATP carrier pr
6	39	13.1	298	1	S03894	ADP,ATP carrier pr
7	39	13.1	298	2	S31814	ADP,ATP carrier pr
8	39	13.1	298	2	B43646	ADP,ATP carrier pr
9	34	11.4	313	2	T23207	hypothetical prote
10	34	11.4	313	2	T25850	hypothetical prote
11	32	10.8	300	2	T25371	hypothetical prote

ALIGNMENTS

RESULT 1  
A44778  
ADP,ATP carrier protein T1 - human  
N/Alternate names: mitochondrial ADP,ATP translocase 1  
C/Species: Homo sapiens (man)  
C/Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
C/Accession: A44778; S03893; A39891; A28116  
R/Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.  
J. Biol. Chem. 264, 13998-14004, 1989  
A/Title: A human muscle adenine nucleotide translocator gene has four exons, is located  
A/Reference number: A44778; MUID:89340499; PMID:2547778  
A/Accession: A44778  
A/Status: preliminary

A/Molecule type: DNA  
A/Residues: 1-298 <LIA>  
A/Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659  
R/Cozens, A.L.; Runswick, M.J.; Walker, J.E.  
J. Mol. Biol. 206, 261-280, 1989  
A/Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tra  
A/Reference number: S03893; MUID:89236396; PMID:2541251  
A/Accession: S03893  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-298 <COZ>  
R/Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987  
A/Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader  
A/Reference number: A39891; MUID:88041149; PMID:2823266  
A/Accession: A39891  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>  
A/Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920  
A/Experimental source: Clone pHMANT  
R/Houldsworth, J.; Attardi, G.  
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
A/Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
A/Reference number: A94197; MUID:88124845; PMID:2829183  
A/Accession: A28116  
A/Molecule type: mRNA  
A/Residues: 1-37 <HOU>  
A/Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725  
A/Experimental source: liver  
C/Genetics:  
A/Gene: GDB:ANT1; T1  
A/Cross-references: GDB:119680; OMIM:103220  
A/Map position: 4Q35-4Q35  
A/Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C/Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
F/2-298/Product: ADP,ATP carrier protein repeat homology <MAT>  
F/5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
F/110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F/207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match	43.8%	Score 130;	DB 1;	Length 298;
Best Local Similarity	100.0%;	Pred. No. 1.5e-120;		
Matches 130;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	17	VAAAVSKTAVAFIERVKLLQVQHASKQISASQYKGIIDCVVRIPKEQGLSFWRGNLA	76	
Db	17	VAAAVSKTAVAFIERVKLLQVQHASKQISASQYKGIIDCVVRIPKEQGLSFWRGNLA	76	
Qy	77	NVIRYFPTQALNFAPKDYKQLFLGGVDRHKQFWRYFAGNLSAGGAAGATSLCFVYVPLDF	136	
Db	77	NVIRYFPTQALNFAPKDYKQLFLGGVDRHKQFWRYFAGNLSAGGAAGATSLCFVYVPLDF	136	
Qy	137	ARTRLAADVG 146		
Db	137	ARTRLAADVG 146		

RESULT 2

S37210  
ADP,ATP carrier protein T1 - mouse  
N/Alternate names: adenine nucleotide carrier  
C/Species: Mus musculus (house mouse)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 20-Aug-1999  
C/Accession: S37210  
R/Laplace, C.; Costet, P.  
submitted to the EMBL Data Library, September 1993  
A/Reference number: S37210  
A/Accession: S37210  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-298 <LIAP>  
A/Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628

## C;Genetics:

A;Gene: ANCL  
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C;Keywords: duplication; transmembrane protein  
F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 26.9%; Score 80; DB 2; Length 298;

Best Local Similarity 100.0%; Pred. No. 4.7e-71;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AAVSXTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77

Db 18 AAVSXTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77

QY 78 VIRYFPTQALNFAFKDKYKQ 97

Db 78 VIRYFPTQALNFAFKDKYKQ 97

## RESULT 3

I60173

adenine nucleotide translocator - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 20-Aug-1999

C;Accession: I60173

R;Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

Biochim. Biophys. Acta 1152, 192-196, 1993

A;Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A;Reference number: I60173; MUID:94002161; PMID:8399300

A;Accession: I60173

A;Status: preliminary; translated from GB/EMBL/DBSJ

A;Molecule type: DNA

A;Residues: 1-298 <RES>

A;Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427

## C;Genetics:

A;Gene: ant1

A;Introns: 37/3; 200/1; 247/1

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C;Keywords: duplication; transmembrane protein

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 26.9%; Score 80; DB 2; Length 298;

Best Local Similarity 100.0%; Pred. No. 4.7e-71;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AAVSXTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77

Db 18 AAVSXTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77

QY 78 VIRYFPTQALNFAFKDKYKQ 97

Db 78 VIRYFPTQALNFAFKDKYKQ 97

## RESULT 4

XWBO

ADP,ATP carrier protein T1 - bovine

N;Alternate names: ADP/ATP translocase T1

C;Species: Bos primigenius taurus (cattle)

C;Date: 14-Nov-1983 #sequence\_revision 22-Jul-1994 #text\_change 22-Jun-1999

C;Accession: A43646; A24822; A03181; A61343; S69369

R;Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

Biochemistry 28, 866-873, 1989

A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in

A;Reference number: A43646; MUID:199229093; PMID:2540808

A;Accession: A43646

A;Molecule type: mRNA

A;Residues: 1-298 <POW>

A;Cross-references: GB:M24102; NID:g529414; PIDN:AAA30768.1; PID:g529415

R;Rasmussen, U.B.; Wohlrab, H.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A;Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual

A;Reference number: A24822; MUID:86295775; PMID:3017341

A;Accession: A24822

A;Molecule type: mRNA

A;Residues: 208-298 <RAS>

A;Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631

R;Aquila, H.; Miera, D.; Eulitz, M.; Klingenberg, M.

Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982

A;Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondria

A;Reference number: A03181; MUID:82188267; PMID:7076130

A;Accession: A03181

A;Molecule type: protein

A;Residues: 2-51,'X',53-70,'X',72-109,'X',111-298 <AQU>

A;Note: residue 52 may be methyllysine

R;Babel, W.; Wächter, E.; Aquila, H.; Klingenberg, M.

Biochim. Biophys. Acta 670, 176-180, 1981

A;Title: Amino acid sequence determination of the ADP,ATP carrier from beef heart mitochr

A;Reference number: A61343; MUID:82046808; PMID:6271240

A;Accession: A61343

A;Molecule type: protein

A;Residues: 205-298 <BAB>

R;Oettmeier, W.; Masson, K.; Kalinna, S.

Eur. J. Biochem. 227, 730-733, 1995

A;Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/

A;Reference number: S69369; MUID:95172058; PMID:7867632

A;Accession: S69369

A;Molecule type: protein

A;Residues: 49-63;154-168 <OET>

C;Comment: This protein is synthesized in the cytosol and transported into the mitochondr

C;Complex: homodimer

C;Function:

A;Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP generat

A;Note: located in the inner mitochondrial membrane

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C;Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochor

F;5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F;110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F;207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

F;2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental

F;52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 25.6%; Score 76; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 4.2e-67;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 SKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLANVIRY 81

Db 22 SKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLANVIRY 81

QY 82 FPTQALNFAFKDKYKQ 97

Db 82 FPTQALNFAFKDKYKQ 97

## RESULT 5

A29132

ADP,ATP carrier protein T2 - human

N;Alternate names: mitochondrial ADP,ATP translocase 2

C;Species: Homo sapiens (man)

C;Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000

C;Accession: A29132; C28116

R;Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.

J. Biol. Chem. 262, 4355-4359, 1987

A;Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulate

A;Reference number: A29132; MUID:87166056; PMID:3031073

A;Accession: A29132

A;Molecule type: mRNA

A;Residues: 1-298 <BAT>

A;Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247

R;Houldsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988



A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
A;Reference number: A94197; MUID:88124845; PMID:2829183  
A;Accession: C28116  
A;Molecule type: mRNA  
A;Residues: 47-65,'G',112-161,'G',163-298 <HOU>  
A;Cross-references: GB:J03591; NID:G339720; PIDN:AAA36749.1; PID:G339721  
A;Experimental source: clone PHAT3  
C;Genetics:  
A;Gene: GDB:ANT2; T3; 2F1  
A;Cross-references: GDB:135190; OMIM:300150  
A;Map position: Xq13-Xq26  
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:  
C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
Query Match 13.1%; Score 39; DB 1; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.8e-30;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146  
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146  
RESULT 6  
ADP/ATP carrier protein T3 - human  
A;Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP/ATP  
C;Species: Homo sapiens (man)  
C;Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
A;Accession: S03894; B28116  
R;Cozens, A.L.; Runswick, M.J.; Walker, J.E.  
J. Mol. Biol. 206, 261-280, 1989  
A;Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr  
A;Reference number: S03893; MUID:89236396; PMID:2541251  
A;Accession: S03894  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-298 <COZ>  
R;Houldsworth, J.; Attardi, G.  
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988  
A;Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a  
A;Reference number: A94197; MUID:88124845; PMID:2829183  
A;Accession: B28116  
A;Molecule type: mRNA  
A;Residues: 36-104,'R',106,'A',109-298 <HOU>  
A;Cross-references: GB:J03592; NID:G339722; PIDN:AAA36750.1; PID:G339723  
A;Experimental source: liver  
C;Genetics:  
A;Gene: GDB:ANT3; ANT3Y  
A;Cross-references: GDB:125184; OMIM:300151; OMIM:403000  
A;Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3  
A;Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:  
C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
F;2-298/Product: ADP/ATP carrier protein #status predicted <MAR>  
F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
Query Match 13.1%; Score 39; DB 1; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.8e-30;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146  
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146  
RESULT 7

S31814  
ADP/ATP carrier protein T2 - mouse  
A;Alternate names: adenine nucleotide translocase  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Apr-1998  
A;Accession: S31814  
R;Costet, P.; Laplace, C.  
submitted to the EMBL Data Library, January 1993  
A;Reference number: S31814  
A;Accession: S31814  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-298 <COS>  
A;Cross-references: EMBL:X70847  
C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
C;Keywords: duplication; transmembrane protein  
F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
Query Match 13.1%; Score 39; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.8e-30;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146  
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146  
RESULT 8  
ADP/ATP carrier protein T2 - bovine  
A;Species: Bos primigenius taurus (cattle)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 20-Aug-1999  
A;Accession: B43646  
R;Powell, S.J.; Mead, S.M.; Runswick, M.J.; Walker, J.E.  
Biochemistry 28, 866-873, 1989  
A;Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in  
A;Reference number: A43646; MUID:89229093; PMID:2540808  
A;Accession: B43646  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-298 <POW>  
C;Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology  
C;Keywords: duplication; homodimer; mitochondrion; transmembrane protein  
F;5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>  
F;110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>  
F;207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>  
Query Match 13.1%; Score 39; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.8e-30;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146  
DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLADVG 146  
RESULT 9  
hypothetical protein K01H12.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000  
C;Accession: T23207  
R;McMurray, A.  
submitted to the EMBL Data Library, December 1995  
A;Reference number: Z19707  
A;Accession: T23207  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-313 <WIL>  
A;Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2

A;Experimental source: clone K01H12

C;Genetics:

A;Gene: CESP:K01H12.2

A;Map position: 4

A;Introns: 4/1; 191/2

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 11.4%; Score 34; DB 2; Length 313;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADV 146

Db 130 FAGNLASGGAAGATSLCFVYPLDFARTRLAADV 163

RESULT 10

T25850

hypothetical protein T01B11.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C;Accession: T25850

R;Geisel, C.; Stellyes, L.

submitted to the EMBL Data Library, December 1996

A;Description: The sequence of C. elegans cosmid T01B11.

A;Reference number: Z20099

A;Accession: T25850

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-313 <GEI>

A;Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4

A;Experimental source: strain Bristol N2; clone T01B11

C;Genetics:

A;Gene: CESP:T01B11.4

A;Map position: 4

A;Introns: 4/1; 191/2

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 11.4%; Score 34; DB 2; Length 313;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAADV 146

Db 130 FAGNLASGGAAGATSLCFVYPLDFARTRLAADV 163

RESULT 11

T25371

hypothetical protein T27E9.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-Jan-2000

C;Accession: T25371

R;Lloyd, C.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z20024

A;Accession: T25371

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-300 <WIL>

A;Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1

A;Experimental source: clone T27E9

C;Genetics:

A;Gene: CESP:T27E9.1

A;Map position: 3

A;Introns: 20/1; 41/3; 115/2

C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 10.8%; Score 32; DB 2; Length 300;

Best Local Similarity 100.0%; Pred. No. 1.5e-23;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 113 FAGNLASGGAAGATSLCFVYPLDFARTRLAAD 144

Db 117 FAGNLASGGAAGATSLCFVYPLDFARTRLAAD 148

Search completed: February 12, 2004, 15:59:06

Job time : 21 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	297	100.0	297	9	US-09-811-094-31	Sequence 31, Appl
2	297	100.0	297	9	US-09-810-644-31	Sequence 31, Appl
3	297	100.0	297	10	US-09-185-904A-31	Sequence 31, Appl
4	39	13.1	298	9	US-09-811-094-32	Sequence 32, Appl
5	39	13.1	298	9	US-09-811-094-33	Sequence 33, Appl
6	39	13.1	298	9	US-09-810-644-32	Sequence 32, Appl
7	39	13.1	298	9	US-09-810-644-33	Sequence 33, Appl
8	39	13.1	298	10	US-09-185-904A-32	Sequence 32, Appl
9	39	13.1	298	10	US-09-185-904A-33	Sequence 33, Appl
10	35	11.8	179	12	US-10-029-386-32501	Sequence 32501, A
11	34	11.4	87	9	US-09-864-761-36440	Sequence 36440, A
12	34	11.4	313	12	US-10-369-493-6072	Sequence 6072, Ap
13	34	11.4	313	12	US-10-369-493-6103	Sequence 6103, Ap
14	32	10.8	300	12	US-10-369-493-5919	Sequence 5919, Ap
15	31	10.4	31	15	US-10-059-261-250	Sequence 250, App

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; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-31

Query Match      100.0%; Score 297; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e-282;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
QY 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
DB 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297

RESULT 3
US-09-185-904A-31
; Sequence 31, Application US/09185904A
; Patent No. US20020171185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yanzhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-31

Query Match      100.0%; Score 297; DB 10; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.4e-282;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60
DB 1 MGDHWSFLKDFLAGAATAAATVAPIERVKLLQVQHASQISAEKQYKGIIDCVVR 60
QY 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
DB 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
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DB 61 IPKEQGLSFWRGNLNANVIRYFTQALNFAFKDKYKQLFLGGVDRHKQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180
QY 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
DB 181 QGIIIRAAAYFGVYDTAKGMLPDPKNVHIFVSWMIAQSVTAVAGLLSYPPDTRRRMMQ 240
QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297
DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKYV 297

RESULT 4
US-09-811-094-32
; Sequence 32, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yanzhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32

Query Match      13.1%; Score 39; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 1e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146
DB 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTLAADV 146

RESULT 5
US-09-811-094-33
; Sequence 33, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yanzhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 33  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-811-094-33

Query Match 13.1%; Score 39; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146  
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146

## RESULT 6

US-09-810-644-32  
; Sequence 32, Application US/09810644  
; Patent No. US20020012992A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Clevenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Willer, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Moos, Walter H.  
; APPLICANT: Pei, Yazhong  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
; FILE REFERENCE: 660088.420D3  
; CURRENT APPLICATION NUMBER: US/09/810.644  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-810-644-32

Query Match 13.1%; Score 39; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146  
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146

## RESULT 7

US-09-810-644-33  
; Sequence 33, Application US/09810644  
; Patent No. US20020012992A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Clevenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Willer, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Moos, Walter H.  
; APPLICANT: Pei, Yazhong  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
; FILE REFERENCE: 660088.420D3  
; CURRENT APPLICATION NUMBER: US/09/810.644  
; CURRENT FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 33

; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-810-644-33

Query Match 13.1%; Score 39; DB 9; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146  
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146

## RESULT 8

US-09-185-904A-32  
; Sequence 32, Application US/09185904A  
; Patent No. US20020177185A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Clevenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Willer, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 660088.420  
; CURRENT APPLICATION NUMBER: US/09/185.904A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-185-904A-32

Query Match 13.1%; Score 39; DB 10; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146  
Db 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146

## RESULT 9

US-09-185-904A-33  
; Sequence 33, Application US/09185904A  
; Patent No. US20020177185A1  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.  
; APPLICANT: Davis, Robert E.  
; APPLICANT: Clevenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Willer, Scott W.  
; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.  
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE  
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: 660088.420  
; CURRENT APPLICATION NUMBER: US/09/185.904A  
; CURRENT FILING DATE: 1998-11-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapien

US-09-185-904A-33

Query Match 13.1%; Score 39; DB 10; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

Db 108 QWRYFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 10

US-10-029-386-32501  
; Sequence 32501, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 32501  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC004000.1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96  
; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 2.00e-83

US-10-029-386-32501

Query Match 11.8%; Score 35; DB 12; Length 179;  
Best Local Similarity 100.0%; Pred. No. 5.3e-26;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 112 YFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

Db 75 YFAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 109

RESULT 11

US-09-864-761-36440  
; Sequence 36440, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 36440  
; LENGTH: 87  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO L78810.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 10  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2  
; OTHER INFORMATION: SWISSPROT HIT: P05141, EVALUE 6.00e-38  
; OTHER INFORMATION: EST\_HUMAN HIT: AW935235.1, EVALUE 5.00e-37

US-09-864-761-36440

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Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 113 FAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 146

Db 1 FAGNLAGGAAGATSLCFVYPLDFARTRLAADVG 34

RESULT 12

US-10-369-493-6072  
; Sequence 6072, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039

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; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6072
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6072

Query Match      11.4%; Score 34; DB 12; Length 313;
Best Local Similarity 100.0%; Pred. No. 8.5e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 FAGNLASGGAAGATSLCFVYPLDPFARTRLAADVG 146
Db 130 FAGNLASGGAAGATSLCFVYPLDPFARTRLAADVG 163

RESULT 13
US-10-369-493-6103
; Sequence 6103, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6103
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6103

Query Match      11.4%; Score 34; DB 12; Length 313;
Best Local Similarity 100.0%; Pred. No. 8.5e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 FAGNLASGGAAGATSLCFVYPLDPFARTRLAADVG 146
Db 130 FAGNLASGGAAGATSLCFVYPLDPFARTRLAADVG 163

RESULT 14
US-10-369-493-5919
; Sequence 5919, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5919
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5919
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Query Match      10.8%; Score 32; DB 12; Length 300;
Best Local Similarity 100.0%; Pred. No. 7.4e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 FAGNLASGGAAGATSLCFVYPLDPFARTRLAAD 144
Db 117 FAGNLASGGAAGATSLCFVYPLDPFARTRLAAD 148

RESULT 15
US-10-059-261-250
; Sequence 250, Application US/10059261
; Publication No. US20030077826A1
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
; APPLICANT: BRIAND, JEAN-PAUL
; TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
; TITLE OF INVENTION: SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
; TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
; TITLE OF INVENTION: (PTPC)
; FILE REFERENCE: 03495.0216
; CURRENT APPLICATION NUMBER: US/10/059,261
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/265,594
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 250
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-059-261-250
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Query Match      10.4%; Score 31; DB 15; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.8e-23;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 DRHKQFWRYFAGNLASGGAAGATSLCFVYPL 134
Db 1 DRHKQFWRYFAGNLASGGAAGATSLCFVYPL 31
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Search completed: February 12, 2004, 15:58:33  
Job time : 34 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2004, 15:54:59 ; Search time 21 Seconds  
(without alignments)  
598.396 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 297  
Sequence: 1 MGDHWSFLKDFLAGAVAA.....LRGMGAFVLVLYDEIKKTV 297

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 30

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	297	100.0	297	4	US-09-434-354-47
2	80	26.9	298	3	US-08-961-871-10
3	39	13.1	298	4	US-09-434-354-48
4	39	13.1	298	4	US-09-434-354-49

ALIGNMENTS

RESULT 1

US-09-434-354-47  
; Sequence 47, Application US/09434354  
; Patent No. 6562563  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Anne N.  
; APPLICANT: Clevenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Andreyev, Alexander Y.  
; APPLICANT: Frigeri, Luciano G.  
; APPLICANT: Velicelebi, Gonul  
; APPLICANT: Davis, Robert E.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
; INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
; IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
; FILE REFERENCE: 660088.433  
; CURRENT APPLICATION NUMBER: US/09/434,354  
; CURRENT FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 47  
; LENGTH: 297  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-434-354-47

Query Match 100.0%; Score 297; DB 4; Length 297;  
Best Local Similarity 100.0%; Pred. No. 4.9e-278;  
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MGDHWSFLKDFLAGAVAAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLNVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
DB 61 IPKEQGLSFWRGNLNVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRYPAGNLASG 120  
QY 121 GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
DB 121 GAAGATSLCFVYPLDFARTRLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
QY 181 QGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSVAAGLLSYFPDTRRRMMMQ 240  
DB 181 QGIIYRAAYFGVYDTAKGMLPDPKNVHIFVSWMTAQSVAAGLLSYFPDTRRRMMMQ 240  
QY 241 SGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKKTV 297  
DB 241 SGRKGADIMYTGTVDCWRKIADGAKAFKGAWSNVLRGMGAFVLVLYDEIKKTV 297

RESULT 2

US-08-961-871-10  
; Sequence 10, Application US/08961871  
; Patent No. 6013858  
; GENERAL INFORMATION:  
; APPLICANT: Wallace, Douglas C.  
; APPLICANT: Graham, Brett H.  
; APPLICANT: Macgregor, Grant R.  
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine  
; Nucleotide Translocator Protein and Methods  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.  
; STREET: 5370 Manhattan Circle, Suite 201  
; CITY: Boulder  
; STATE: Colorado  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,871  
; FILING DATE: 31-OCT-1997  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/030,017  
; FILING DATE: 01-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ferber, Donna M.  
; REGISTRATION NUMBER: 33,878  
; REFERENCE/DOCKET NUMBER: 78-96  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 499-8080  
; TELEFAX: (303) 499-8089  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 298 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-871-10

Query Match      26.9%; Score 80; DB 3; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.7e-69;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 AAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPEQGFSLFWRGNLN 77
Db 18 AAASKTAVAPIERVKLLQVQHASKOISAEKQYKGIIDCVRIKPEQGFSLFWRGNLN 77
Qy 78 VIRYFPTQALNFAFKDKYKQ 97
Db 78 VIRYFPTQALNFAFKDKYKQ 97

RESULT 3
US-09-434-354-48
; Sequence 48, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-48

Query Match      13.1%; Score 39; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.4e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146
Db 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 4
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; Sequence 49, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 49
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-49

Query Match      13.1%; Score 39; DB 4; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.4e-29;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146
Db 108 QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

Search completed: February 12, 2004, 15:57:46
Job time : 21 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2004, 15:54:54 ; Search time 41 Seconds  
(without alignments)  
1149.800 Million cell updates/sec

Title: US-09-809-827-31

Perfect score: 297

Sequence: 1 MGDHAWFLKDFLAGAVAAA.....LRMGAGFVLVLYDEIKYV 297

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 30

Total number of hits satisfying chosen parameters: 36

Minimum DB seq length: 0

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- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	297	100.0	297	21	AAU01199 Human adenine nucl
2	297	100.0	297	22	AAU01200 Human adenine nucl
3	297	100.0	297	23	AAU01378 Human adenine nucl
4	80	26.9	293	22	ABU53219 Human metabolism-a
5	80	26.9	298	19	AAW61169 Anti protein Mus
6	39	13.1	283	22	ABG27056 Novel human diagno
7	39	13.1	298	21	AAU01032 Human adenine nucl
8	39	13.1	298	21	AAU01033 Human adenine nucl
9	39	13.1	298	22	AAU01034 Human polypeptide

10	39	13.1	298	22	AAU01199 Human adenine nucl
11	39	13.1	298	22	AAU01200 Human adenine nucl
12	39	13.1	298	23	AAU01378 Human insulin rece
13	39	13.1	298	23	AAU01379 Human adenine nucl
14	39	13.1	298	23	AAU01380 Human adenine nucl
15	39	13.1	323	22	AAU01427 Human polypeptide
16	39	13.1	429	24	ABR41715 Human DTHP organe
17	37	12.5	299	22	ABR66082 Drosophila melanog
18	37	12.5	299	22	ABR66700 Human liver peptid
19	34	11.4	87	22	ABG50570 Peptide #3200 enco
20	34	11.4	87	22	ABR30549 Peptide #3220 enco
21	34	11.4	87	22	ABR35714 Protein #3141 enco
22	34	11.4	87	22	ABR21142 Human brain expres
23	34	11.4	87	22	AAU56523 Human bone marrow
24	34	11.4	87	22	AAU68905 Peptide #3162 enco
25	34	11.4	87	22	AAU16728 Peptide #3253 enco
26	34	11.4	87	22	AAU29216 Peptide #3127 enco
27	34	11.4	87	22	AAU04445 Human peptide enco
28	34	11.4	87	23	ABG38486 Drosophila melanog
29	34	11.4	307	22	ABR58380 PTPC-interacting T
30	31	10.4	31	23	ABP56153 PTPC-interacting S
31	31	10.4	31	23	ABP56167 Human metabolism-a
32	31	10.4	315	22	ABU53218 Human TRICH-19 pro
33	31	10.4	315	23	AAE21175 Novel human diagno
34	31	10.4	325	22	ABG15423 Novel human diagno
35	30	10.1	136	22	ABG18921 Human ovarian anti
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ALIGNMENTS

RESULT 1  
AAU71031  
ID AAU71031 standard; Protein; 297 AA.

AC AAU71031;

DT 29-AUG-2000 (first entry)

XX Human adenine nucleotide translocator ANTL.

XX Human; adenine nucleotide translocator; ANTL; mitochondria; ADP; ATP;  
XX adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
XX mitochondrial permeability transition; neuroprotective; neuroleptic;  
XX antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
XX antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;  
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; dactylia;  
XX diabetes; Leber's hereditary optic neuropathy; lactic acidosis; stroke; MIDD;  
XX mitochondrial encephalopathy; deafness; hyperproliferative disorder;  
XX myoclonic epilepsy red ragged fibre syndrome.

OS Homo sapiens.

XX WO2000026370-A2.

PD 11-MAY-2000.

XX 03-NOV-1999; 99WO-US25883.

XX 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;

PI Ghosh SS;

XX WPI; 2000-365619/31.

DR N-PSDB; AAD00519.

XX Recombinant construct encoding adenine nucleotide translocator

PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 XX against mitochondrial disease -  
 PS Claim 44; Page 172; 175pp; English.  
 XX The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANTL1 from human brain.

XX Sequence 297 AA;  
 SQ  
 Query Match 100.0%; Score 297; DB 21; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-274;  
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGDHWSFLKDFLAGAATAVSTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
 DB 1 MGDHWSFLKDFLAGAATAVSTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRVFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRVFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYFPDTRRRMMMQ 240  
 DB 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYFPDTRRRMMMQ 240  
 QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLKRGMGAFVLVLYDEIKKYV 297  
 DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLKRGMGAFVLVLYDEIKKYV 297

RESULT 2  
 AAU01198  
 ID AAU01198 standard; Protein; 297 AA.  
 XX AAU01198;  
 AC AAU01198;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX Human adenine nucleotide translocator-1 (ANT-1) protein.  
 DE  
 XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200132876-A2.  
 PN  
 XX  
 XX 10-MAY-2001.  
 PD  
 XX  
 XX 03-NOV-2000; 2000WO-US30535.  
 PF  
 XX

PR 03-NOV-1999; 99US-0434354.  
 XX (MITO-) MITOKOR.  
 PA  
 XX Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri IG;  
 PI Velicelcibi G, Davis RE;  
 XX WPI; 2001-291054/30.  
 DR N-PSDB; AAS05901.  
 DR  
 XX New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 XX Disclosure; Fig 2; 186pp; English.  
 PS  
 XX The present sequence represents human adenine nucleotide translocator-1  
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability  
 CC transition (MTP) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 297 AA;  
 SQ  
 Query Match 100.0%; Score 297; DB 22; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-274;  
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGDHWSFLKDFLAGAATAVSTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
 DB 1 MGDHWSFLKDFLAGAATAVSTAVPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
 QY 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRVFAGNLASG 120  
 DB 61 IPKEQGLSFWRGNLANVIRYPTQALNPAFKDKYKQLFLGGVDRHKQFWRVFAGNLASG 120  
 QY 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
 DB 121 GAAGATSLCFVYPLDFARTLAADVGRRAQREPHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
 QY 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYFPDTRRRMMMQ 240  
 DB 181 QGIIIVRAAYFGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYFPDTRRRMMMQ 240  
 QY 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLKRGMGAFVLVLYDEIKKYV 297  
 DB 241 SGRKGADIMYTGTVDCWRKIAKDEGAKAFKPGAWSNVLKRGMGAFVLVLYDEIKKYV 297

RESULT 3  
 AAU10378  
 ID AAU10378 standard; Protein; 297 AA.  
 XX AAU10378;  
 AC AAU10378;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX Human adenine nucleotide translocator 1 (ANT1).  
 DE

XX Human; adenine nucleotide translocator; ANT;  
KW mitochondrial matrix protein.  
XX Homo sapiens.  
XX WO200185944-A2.  
XX 15-NOV-2001.  
XX 11-MAY-2001; 2001WO-US15416.  
XX 11-MAY-2000; 2000US-0569327.  
XX (MITO-) MITOKOR.  
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;  
XX WPI; 2002-055598/07.  
DR N-PSDB; AAS16688.  
XX Novel recombinant expression construct for producing adenine nucleotide  
PT translocator polypeptides, comprises a regulated promoter linked to  
PT nucleic acid encoding the polypeptide  
XX Claim 44; Fig 2; 147pp; English.  
XX The invention relates to a recombinant expression construct (I)  
CC comprising a regulated promoter operably linked to a nucleic acid  
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
CC culturing the host cell. (I) is also useful for targeting a polypeptide  
CC of interest to a mitochondrial membrane, where ANT polypeptide is  
CC expressed as a fusion protein with the polypeptide of interest.  
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
CC ligand is useful for determining the presence of an ANT polypeptide.  
CC Preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
CC ANT from a biological sample, where the ANT ligand is covalently or non-  
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
CC useful for identifying an agent that interacts with an ANT polypeptide.  
CC The present sequence represents the amino acid sequence of human ANT1.  
XX SQ Sequence 297 AA;  
Query Match 100.0%; Score 297; DB 23; Length 297;  
Best Local Similarity 100.0%; Pred. No. 2.7e-274;  
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MGDHANSFLKDFLAGAANAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
DB 1 MGDHANSFLKDFLAGAANAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVR 60  
QY 61 IPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLASG 120  
DB 61 IPKEQGLSFWRGNLANVIRYFPTQALNFAFKDKYKOLFGLGGVDRHKQFWRYPAGNLASG 120  
QY 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
DB 121 GAAGATSLCFVYPLDFAARTLAADVGRRAQREFHGLGDCIIKIFKSDGLRGLYQGFNVSV 180  
QY 181 QGIIIIYRAAYFGVYDTAKMLPDPKNVHIFVSNMIAQSVTAVAGLLSYPPDTRRRMMQ 240  
DB 181 QGIIIIYRAAYFGVYDTAKMLPDPKNVHIFVSNMIAQSVTAVAGLLSYPPDTRRRMMQ 240  
QY 241 SGRKGADIMYTGTVDCWRKTADEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKYV 297  
DB 241 SGRKGADIMYTGTVDCWRKTADEGAKAFKFGAWSNVLRGMGAFVLVLYDEIKYV 297

RESULT 4  
ABUS3219  
ID ABUS3219 standard; Protein; 293 AA.  
XX AC ABUS3219;  
XX DT 14-APR-2003 (first entry)  
XX DE Human metabolism-associated DKFZphtes3\_35n12 homologue #1.  
XX KW Human; gene therapy; vaccine; disease treatment; detection.  
XX OS Homo sapiens.  
XX PN WO200112659-A2.  
XX PD 22-FEB-2001.  
XX PF 18-AUG-2000; 2000WO-IB01496.  
XX PR 18-AUG-1999; 99US-0149499.  
XX PR 28-SEP-1999; 99US-0156503.  
XX PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
XX PI Wiemann S;  
XX WPI; 2001-327840/34.  
XX Nucleic acids having the sequences of clones isolated from libraries of  
XX different human tissues, useful in recombinant DNA methodologies -  
XX Example III; Page 850; 1095pp; English.  
XX This invention describes novel polynucleotides and polypeptides isolated  
XX from human cDNA libraries which can be used for gene therapy or in  
XX vaccines. The polynucleotides of the invention and antibodies encoded by  
XX them may be used in the prevention, diagnosis and treatment of diseases  
XX associated with inappropriate polypeptide expression. The products of the  
XX invention may also be used to identify modulators of expression and  
XX activity and to down regulate expression and activity. The antibodies of  
XX the invention may also be used as diagnostic agents for detecting the  
XX presence of polypeptides in samples. This sequence represents a homologue  
XX of a polypeptide described in the disclosure of the invention.  
XX SQ Sequence 293 AA;  
Query Match 26.9%; Score 80; DB 22; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1e-67;  
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 18 AAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 77  
DB 14 AAASVTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGLSFWRGNLAN 73  
QY 78 VIRYPTQALNFAFKDKYKQ 97  
DB 74 VIRYPTQALNFAFKDKYKQ 93  
RESULT 5  
AAW61169  
ID AAW61169 standard; Protein; 298 AA.  
XX AC AAW61169;  
XX DT 28-SEP-1998 (first entry)  
XX DE Ant1 protein.  
XX KW Ant1; Adenine nucleotide translocator; cloning; screening;  
KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;  
KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;

KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;  
 KW lactic acidosis; degenerative muscle disease.  
 XX Mus sp.  
 XX WO9819714-A1.  
 XX 14-MAY-1998.  
 XX 31-OCT-1997; 97WO-US19882.  
 XX 01-NOV-1996; 96US-0030017.  
 XX (UYEM-) UNIV EMORY.  
 XX Graham BC, Macgregor GR, Wallace DC;  
 XX MPI; 1998-286608/25.  
 XX N-PSDB; AAV36479.  
 XX Mice lacking heart-muscle adenine nucleotide translocator protein -  
 PT useful as model for mitochondrial myopathy and hypertrophic  
 PT cardiomyopathy in animals and to test therapeutic compositions or  
 PT gene therapies  
 XX Disclosure; Page 39-40; 61pp; English.  
 XX The present sequence is the mouse Ant1 protein, the cDNA producing this  
 CC polypeptide is cloned by screening a mouse heart cDNA library with the  
 CC human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA  
 CC tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by  
 CC the Ant1 locus, a nuclear gene on chromosome 8. This protein is required  
 CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP  
 CC which can then be converted into ATP. An Ant1 homozygous mutant would  
 CC thus be defective in OXPHOS which results in disease in oxidative  
 CC metabolism dependent tissues. This mouse Ant1 homozygous mutant can be  
 CC used as a model system for fascioscapular humeral muscular dystrophy,  
 CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model  
 CC systems can be used to test possible therapeutic compounds which  
 CC increase/mediate ATP and ADP exchange across the mitochondrial membrane  
 CC independent of ANT1.  
 XX Sequence 298 AA;  
 SQ Query Match 26.9%; Score 80; DB 19; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-67;  
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 18 AAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77  
 DB 18 AAVSKTAVAPIERVKLLQVHASKQISAEKQYKGIIDCVVRIPKEQGFLSFWRGNLAN 77  
 QY 78 VIRYFPTQALNFAFKDKYKQ 97  
 DB 78 VIRYFPTQALNFAFKDKYKQ 97  
 RESULT 6  
 ABG27056  
 ID ABG27056 standard; Protein; 263 AA.  
 XX  
 AC ABG27056;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Novel human diagnostic protein #27047.  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.  
 OS  
 XX WO200175067-A2.  
 PN

XX 11-OCT-2001.  
 XX 30-MAR-2001; 2001WO-US08631.  
 XX 31-MAR-2000; 2000US-0540217.  
 PR 23-AUG-2000; 2000US-0649167.  
 XX (HYSE-) HYSEQ INC.  
 PA Drmanac RT, Liu C, Tang YT;  
 XX MPI; 2001-639362/73.  
 DR N-PSDB; AAS91243.  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity  
 XX Claim 20; SEQ ID No 57415; 103pp; English.  
 PS The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 263 AA;  
 Query Match 13.1%; Score 39; DB 22; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 1e-28;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 108 QFWRYFAGNLASGGAGATSLCFVYPLDFARTRLAADV 146  
 DB 108 QFWRYFAGNLASGGAGATSLCFVYPLDFARTRLAADV 146  
 RESULT 7  
 AAY71032  
 ID AAY71032 standard; Protein; 298 AA.  
 XX  
 AC AAY71032;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Human adenine nucleotide translocator ANT2.  
 XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;  
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
 KW mitochondrial permeability transition; neuroprotective; nootropic;  
 KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
 KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;

KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
 KW myoclonic epilepsy red ragged fibre syndrome.

OS Homo sapiens.

PN WO200026370-A2.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-US25883.

XX 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS;

DR WPI; 2000-365619/31.

DR N-PSDB; AAD00520.

XX Recombinant construct encoding adenine nucleotide translocator

PT polypeptide, useful e.g. in screening for potential therapeutic agents

PT against mitochondrial disease -

XX Claim 45; Page 172-173; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, hyperproliferative  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT2 from human brain.

XX Sequence 298 AA;

Query Match 13.1%; Score 39; DB 21; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.1e-28;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYPAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

DB 108 QFWRYPAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 8

AA771033

ID AAY71033 standard; Protein; 298 AA.

XX AAY71033;

XX 29-AUG-2000 (first entry)

XX Human adenine nucleotide translocator ANT3.

XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;  
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
 KW mitochondrial permeability transition; neuroprotective; nontropic;  
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
 KW antipeptidic; cerebroprotective; therapeutic; screening; psoriasis;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;

KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
 KW myoclonic epilepsy red ragged fibre syndrome.

OS Homo sapiens.

PN WO200026370-A2.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-US25883.

XX 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS;

DR WPI; 2000-365619/31.

DR N-PSDB; AAD00521.

XX Recombinant construct encoding adenine nucleotide translocator

PT polypeptide, useful e.g. in screening for potential therapeutic agents

PT against mitochondrial disease -

XX Claim 46; Page 173-174; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine  
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves  
 CC as an important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,  
 CC Leber's hereditary optic neuropathy, schizophrenia, hyperproliferative  
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative  
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic  
 CC epilepsy red ragged fibre syndrome. The present sequence is an  
 CC adenine nucleotide translocator ANT3 from human brain.

XX Sequence 298 AA;

Query Match 13.1%; Score 39; DB 21; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.1e-28;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 QFWRYPAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

DB 108 QFWRYPAGNLASGGAAGATSLCFVYPLDFARTRLAADVG 146

RESULT 9

AAM39641

ID AAM39641 standard; Protein; 298 AA.

XX AAM39641;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 2786.

XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR N-PSDB; AAI58797.  
 XX  
 XX Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Example 4; SEQ ID NO 2786; 10078pp; English.  
 XX  
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemia and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 13.1%; Score 39; DB 22; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAVDG 146  
 DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAVDG 146  
 RESULT 10  
 AAU01199  
 ID AAU01199 standard; Protein; 298 AA.  
 XX  
 AC AAU01199;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.  
 XX  
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;  
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;

KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200132876-A2.  
 XX  
 PD 10-MAY-2001.  
 XX  
 PF 03-NOV-2000; 2000WO-US30535.  
 XX  
 PR 03-NOV-1999; 99US-0434354.  
 XX  
 PA (MITO-) MITOKOR.  
 XX  
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;  
 PI Velicelebi G, Davis RE;  
 XX  
 DR WPI; 2001-291054/30.  
 DR N-PSDB; AAS05902.  
 XX  
 XX New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
 PT fused to energy transfer molecule -  
 XX  
 PS Disclosure; Fig 2; 186pp; English.  
 XX  
 CC The present sequence represents human adenine nucleotide translocator-2  
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability  
 CC transition (MTP) pore components responsible for mediating transport  
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
 CC with other mitochondrial core components e.g. cyclophilins to  
 CC regulate MPT. The present invention relates to a novel nucleic acid  
 CC expression construct comprising a promoter operably linked to a  
 CC polynucleotide encoding a mitochondrial pore component polypeptide  
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
 CC expression construct can alter mitochondrial membrane permeability  
 CC transition and/or alter the interaction between mitochondrial core  
 CC components. The methods are useful for screening for agents that alter  
 CC MPT and/or cell survival. These agents are useful for the prevention or  
 CC treatment of diseases associated with altered mitochondrial function or  
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
 CC mitochondrial encephalopathy, lactic acidosis, stroke,  
 CC hyperproliferative disorders e.g. cancer, and deafness.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 13.1%; Score 39; DB 22; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAVDG 146  
 DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAVDG 146  
 RESULT 11  
 AAU01200  
 ID AAU01200 standard; Protein; 298 AA.  
 XX  
 AC AAU01200;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.  
 XX  
 KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;



KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.  
XX Homo sapiens.  
XX WO200132876-A2.  
XX PD 10-MAY-2001.  
XX 03-NOV-2000; 2000WO-US30535.  
XX PF 03-NOV-1999; 99US-0434354.  
XX PR 03-NOV-1999; 99US-0434354.  
XX PA (MITO-) MITOKOR.  
XX  
XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;  
PI Velicelebi G, Davis RE;  
XX  
XX WPI: 2001-291054/30.  
DR N-PSDB; AA505903.  
XX  
XX New nucleic acid expression constructs, useful for screening for agents  
PT that alter mitochondrial permeability transition (MPT), comprises  
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide  
PT fused to energy transfer molecule -  
XX  
PS Disclosure; Fig 2; 186pp; English.  
XX  
XX The present sequence represents human adenine nucleotide translocator-3  
CC (ANT-3) protein. ANT proteins are mitochondrial permeability  
CC transition (MTP) pore components responsible for mediating transport  
CC of ADP across the mitochondrial inner membrane. ANT proteins interact  
CC with other mitochondrial core components e.g. cyclophilins to  
CC regulate MPT. The present invention relates to a novel nucleic acid  
CC expression construct comprising a promoter operably linked to a  
CC polynucleotide encoding a mitochondrial pore component polypeptide  
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein  
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel  
CC expression construct can alter mitochondrial membrane permeability  
CC transition and/or alter the interaction between mitochondrial core  
CC components. The methods are useful for screening for agents that alter  
CC MPT and/or cell survival. These agents are useful for the prevention or  
CC treatment of diseases associated with altered mitochondrial function or  
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes  
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,  
CC mitochondrial encephalopathy, lactic acidosis, stroke,  
CC hyperproliferative disorders e.g. cancer, and deafness.  
XX  
SQ Sequence 298 AA;  
Query Match 13.1%; Score 39; DB 22; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDPARTRLAADVG 146  
Db |||||  
108 QFWRYFAGNLASGGAAGATSLCFVYPLDPARTRLAADVG 146  
RESULT 12  
AA018516  
ID AA018516 standard; Protein; 298 AA.  
XX  
XX AA018516;  
XX  
DT 11-OCT-2002 (first entry)  
XX  
XX Human insulin receptor signaling modifier SEQ ID NO: 54.  
XX  
XX Human; insulin receptor signaling; insulin receptor signaling modifier;  
KW ISM; diabetes; metabolic syndrome; antidiabetic.  
XX  
XX Homo sapiens.  
OS  
XX

PN WO200255664-A2.  
XX  
XX PD 18-JUL-2002.  
XX  
XX PF 11-JAN-2002; 2002WO-US01048.  
XX  
XX PR 12-JAN-2001; 2001US-261226P.  
PR 12-JAN-2001; 2001US-261303P.  
PR 12-JAN-2001; 2001US-261304P.  
PR 12-JAN-2001; 2001US-261335P.  
PR 12-JAN-2001; 2001US-261336P.  
PR 12-JAN-2001; 2001US-261361P.  
PR 12-JAN-2001; 2001US-261456P.  
PR 12-JAN-2001; 2001US-261457P.  
PR 12-JAN-2001; 2001US-261458P.  
PR 12-JAN-2001; 2001US-261459P.  
PR 12-JAN-2001; 2001US-261461P.  
PR 12-JAN-2001; 2001US-261518P.  
PR 12-JAN-2001; 2001US-261531P.  
PR 12-JAN-2001; 2001US-261532P.  
PR 12-JAN-2001; 2001US-261589P.  
PR 12-JAN-2001; 2001US-261590P.  
PR 12-JAN-2001; 2001US-261694P.  
PR 12-JAN-2001; 2001US-261695P.  
PR 12-JAN-2001; 2001US-261697P.  
XX  
XX (EXEL-) EXELIXIS INC.  
XX  
XX Seidel-Dugan C, Ferguson KC, Kidd T;  
PI WPI: 2002-599664/64.  
XX N-PSDB; AAL48635.  
XX  
XX Identifying an insulin receptor signaling modulator, useful as drug  
PT targets for treating diabetes or metabolic disorders, comprises  
PT contacting an assay system comprising insulin receptor signaling  
PT modifiers with a test agent -  
XX  
PS Disclosure; Page 160-161; 232pp; English.  
XX  
XX The present invention relates to a method of identifying a candidate  
CC insulin receptor (INR) signaling modulating agent, involving contacting  
CC an assay system comprising an insulin receptor signaling modifier (ISM)  
CC polypeptide or nucleic acid with a test agent, and detecting a test  
CC agent-biased activity of the assay system. The method is useful for  
CC identifying candidate INR signaling modulating agents. ISM genes may be  
CC used as drug targets for treatment of disorders related to INR signaling  
CC such as diabetes or metabolic syndrome. ISM nucleic acids and  
CC polypeptides are useful for identifying and testing agents that modulate  
CC ISM function and for other applications related to the involvement of ISM  
CC in INR signaling, and for identifying subjects having a predisposition to  
CC such diseases associated with INR signaling. The present sequence is an  
CC ISM protein described in the exemplification of the invention.  
XX  
SQ Sequence 298 AA;  
Query Match 13.1%; Score 39; DB 23; Length 298;  
Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLASGGAAGATSLCFVYPLDPARTRLAADVG 146  
Db |||||  
108 QFWRYFAGNLASGGAAGATSLCFVYPLDPARTRLAADVG 146  
RESULT 13  
AAU10379  
ID AAU10379 standard; Protein; 298 AA.  
XX  
XX AAU10379;  
XX  
XX 14-FEB-2002 (first entry)  
XX

DE Human adenine nucleotide translocator 2 (ANT2).  
 XX  
 KW Human; adenine nucleotide translocator; ANT; ss;  
 KW mitochondrial matrix protein.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200185944-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 11-MAY-2001; 2001WO-US15416.  
 XX  
 PR 11-MAY-2000; 2000US-0569327.  
 XX  
 PA (MITO-) MITOKOR.  
 XX  
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;  
 XX  
 DR WPI: 2002-055598/07.  
 DR N-PSDB; AAS16689.  
 XX  
 XX Novel recombinant expression construct for producing adenine nucleotide  
 PT translocator polypeptides, comprises a regulated promoter linked to  
 PT nucleic acid encoding the polypeptide -  
 XX  
 PS Claim 44; Fig 2; 147pp; English.  
 XX  
 XX The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide, ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT2.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 13.1%; Score 39; DB 23; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAADV 146  
 DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAADV 146  
 RESULT 14  
 AAU10380  
 ID AAU10380 standard; Protein; 298 AA.  
 XX  
 AC AAU10380;  
 XX  
 XX 14-FEB-2002 (first entry)  
 DT  
 DE Human adenine nucleotide translocator 3 (ANT3).  
 XX  
 KW Human; adenine nucleotide translocator; ANT;  
 KW mitochondrial matrix protein.  
 XX  
 OS Homo sapiens.  
 XX

PN WO200185944-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 11-MAY-2001; 2001WO-US15416.  
 XX  
 PR 11-MAY-2000; 2000US-0569327.  
 XX  
 PA (MITO-) MITOKOR.  
 XX  
 XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;  
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;  
 XX  
 DR WPI: 2002-055598/07.  
 DR N-PSDB; AAS16690.  
 XX  
 XX Novel recombinant expression construct for producing adenine nucleotide  
 PT translocator polypeptides, comprises a regulated promoter linked to  
 PT nucleic acid encoding the polypeptide -  
 XX  
 PS Example 3; Fig 2; 147pp; English.  
 XX  
 XX The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide, ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the amino acid sequence of human ANT3.  
 XX  
 SQ Sequence 298 AA;  
 Query Match 13.1%; Score 39; DB 23; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-28;  
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAADV 146  
 DB 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTLAAADV 146  
 RESULT 15  
 AAM41427  
 ID AAM41427 standard; Protein; 323 AA.  
 XX  
 AC AAM41427;  
 XX  
 XX 22-OCT-2001 (first entry)  
 DT  
 DE Human polypeptide SEQ ID NO 6358.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.  
XX  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX  
DR WPI; 2001-442253/47.  
DR N-PSDB; AAI60583.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders  
PT such as central nervous system injuries -  
XX  
PS Example 2; SEQ ID NO 6358; 10078pp; English.  
XX  
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and  
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification.  
XX  
SQ Sequence 323 AA;  
Query Match 13.1%; Score 39; DB 22; Length 323;  
Best Local Similarity 100.0%; Pred. No. 1.2e-28;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 108 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 146  
Db 133 QFWRYFAGNLAGGAGATSLCFVYPLDFARTRLAADV 171  
Search completed: February 12, 2004, 15:55:50  
Job time : 42 secs

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